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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/079,384

DATE: 07/29/2002 8.6
TIME: 13:32:10

Input Set : A:\Seq listing 9409-2135.txt

Output Set: N:\CRF3\07292002\J079384.raw

3 <110> APPLICANT: Communi, Didier
5 <120> TITLE OF INVENTION: COMPOSITIONS AND METHODS COMPRISING G-PROTEIN COUPLED RECEPTORS

7 <130> FILE REFERENCE: 9409/2132

9 <140> CURRENT APPLICATION NUMBER: US 10/079,384

10 <141> CURRENT FILING DATE: 2002-02-20

12 <150> PRIOR APPLICATION NUMBER: US 09/885,453

13 <151> PRIOR FILING DATE: 2001-06-20

15 <160> NUMBER OF SEQ ID NOS: 50

17 <170> SOFTWARE: PatentIn version 3.1

19 <210> SEQ ID NO: 1

20 <211> LENGTH: 1356

21 <212> TYPE: DNA

22 <213> ORGANISM: Homo sapiens

24 <220> FEATURE:

25 <221> NAME/KEY: CDS

26 <222> LOCATION: (1)..(1356)

27 <223> OTHER INFORMATION:

29 <400> SEQUENCE: 1

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32	1 5 10 15	
34	ggg agg gtc cct caa acc cca ggt ccc tct act gcc agt ggg gtc ccg	96
35	Gly Arg Val Pro Gln Thr Pro Gly Pro Ser Thr Ala Ser Gly Val Pro	
36	20 25 30	
38	gaq gtg ggg cta cgg gat gtt gct tgc gaa tct gtg gcc ctc ttc ttc	144
39	Glu Val Gly Leu Arg Asp Val Ala Ser Glu Ser Val Ala Leu Phe Phe	
40	35 40 45	
42	atg ctc ctg ctg gac ttg act gct gtg gct ggc aat gcc gct gtg atg	192
43	Met Leu Leu Leu Asp Leu Thr Ala Val Ala Gly Asn Ala Ala Val Met	
44	50 55 60	
46	gcc gtg atc gcc aag acg cct gcc ctc cga aaa ttt gtc ttc gtc ttc	240
47	Ala Val Ile Ala Lys Thr Pro Ala Leu Arg Lys Phe Val Phe Val Phe	
48	65 70 75 80	
50	cac ctc tgc ctg gtg gac ctg ctg gct gcc ctg acc ctc atg ccc ctg	288
51	His Leu Cys Leu Val Asp Leu Leu Ala Ala Leu Thr Leu Met Pro Leu	
52	85 90 95	
54	gcc atg ctc tcc agc tct gcc ctc ttt gac cac gcc ctc ttt ggg gag	336
55	Ala Met Leu Ser Ser Ser Ala Leu Phe Asp His Ala Leu Phe Gly Glu	
56	100 105 110	
58	gtg gcc tgc cgc ctc tac ttg ttt ctg agc gtg tgc ttt gtc agc ctg	384
59	Val Ala Cys Arg Leu Tyr Leu Phe Leu Ser Val Cys Phe Val Ser Leu	
60	115 120 125	
62	gcc atc ctc tgc gtg tca gcc atc aat gtg gag cgc tac tat tac gta	432

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63	Ala	Ile	Leu	Ser	Val	Ser	Ala	Ile	Asn	Val	Glu	Arg	Tyr	Tyr	Tyr	Val	
64		130					135				140						
66	gtc	cac	ccc	atg	cgc	tac	gag	gtg	cgc	atg	acg	ctg	ggg	ctg	gtg	gcc	480
67	Val	His	Pro	Met	Arg	Tyr	Glu	Val	Arg	Met	Thr	Leu	Gly	Leu	Val	Ala	
68	145					150				155				160			
70	tct	gtg	ctg	gtg	ggt	gtg	tgg	gtg	aag	gcc	ttg	gcc	atg	gct	tct	gtg	528
71	Ser	Val	Leu	Val	Gly	Val	Trp	Val	Lys	Ala	Leu	Ala	Met	Ala	Ser	Val	
72					165					170				175			
74	cca	gtg	ttg	gga	agg	gtc	tcc	tgg	gag	gaa	gga	gct	ccc	agt	gtc	ccc	576
75	Pro	Val	Leu	Gly	Arg	Val	Ser	Trp	Glu	Glu	Gly	Ala	Pro	Ser	Val	Pro	
76			180						185				190				
78	cca	ggc	tgt	tca	ctc	cag	tgg	agc	cac	agt	gcc	tac	tgc	cag	ctt	ttt	624
79	Pro	Gly	Cys	Ser	Leu	Gln	Trp	Ser	His	Ser	Ala	Tyr	Cys	Gln	Leu	Phe	
80			195				200						205				
82	gtg	gtg	gtc	ttt	gct	gtc	ctt	tac	ttt	ctg	ttg	ccc	ctg	ctc	ctc	ata	672
83	Val	Val	Val	Phe	Ala	Val	Leu	Tyr	Phe	Leu	Leu	Pro	Leu	Leu	Leu	Ile	
84		210				215				220							
86	ctt	gtg	gtc	tac	tgc	agc	atg	ttc	cga	gtg	gcc	cgc	gtg	gct	gcc	atg	720
87	Leu	Val	Val	Tyr	Cys	Ser	Met	Phe	Arg	Val	Ala	Arg	Val	Ala	Ala	Met	
88	225				230				235				240				
90	cag	cac	ggg	ccg	ctg	ccc	acg	tgg	atg	gag	aca	ccc	cgg	caa	cgc	tcc	768
91	Gln	His	Gly	Pro	Leu	Pro	Thr	Trp	Met	Glu	Thr	Pro	Arg	Gln	Arg	Ser	
92			245				250			255							
94	gaa	tct	ctc	agc	agc	cgc	tcc	acg	atg	gtc	acc	agc	tcg	ggg	gcc	ccc	816
95	Glu	Ser	Leu	Ser	Ser	Arg	Ser	Thr	Met	Val	Thr	Ser	Ser	Gly	Ala	Pro	
96			260				265						270				
98	cag	acc	acc	cca	cac	cgg	acg	ttt	ggg	gga	ggg	aaa	gca	gca	gtg	gtt	864
99	Gln	Thr	Thr	Pro	His	Arg	Thr	Phe	Gly	Gly	Gly	Lys	Ala	Ala	Val	Val	
100		275				280				285							
102	ctc	ctg	gct	gtg	ggg	gga	cag	ttc	ctg	ctc	tgt	tgg	ttg	ccc	tac	ttc	912
103	Leu	Leu	Ala	Val	Gly	Gly	Gln	Phe	Leu	Leu	Cys	Trp	Leu	Pro	Tyr	Phe	
104		290				295				300							
106	tct	ttc	cac	ctc	tat	gtt	gcc	ctg	agt	gct	cag	ccc	att	tca	act	ggg	960
107	Ser	Phe	His	Leu	Tyr	Val	Ala	Leu	Ser	Ala	Gln	Pro	Ile	Ser	Thr	Gly	
108	305				310				315				320				
110	cag	gtg	gag	agt	gtg	gtc	acc	tgg	att	ggc	tac	ttt	tgc	ttc	act	tcc	1008
111	Gln	Val	Glu	Ser	Val	Val	Thr	Trp	Ile	Gly	Tyr	Phe	Cys	Phe	Thr	Ser	
112			325				330			335							
114	aac	cct	ttc	ttc	tat	gga	tgt	ctc	aac	cgg	cag	atc	cgg	ggg	gag	ctc	1056
115	Asn	Pro	Phe	Phe	Tyr	Gly	Cys	Leu	Asn	Arg	Gln	Ile	Arg	Gly	Glu	Leu	
116			340				345					350					
118	agc	aag	cag	ttt	gtc	tgc	ttc	ttc	aag	cca	gct	cca	gag	gag	gag	ctg	1104
119	Ser	Lys	Gln	Phe	Val	Cys	Phe	Phe	Lys	Pro	Ala	Pro	Glu	Glu	Glu	Leu	
120		355				360				365							
122	agg	ctg	cct	agc	cgg	gag	ggc	tcc	att	gag	gag	aac	ttc	ctg	cag	ttc	1152
123	Arg	Leu	Pro	Ser	Arg	Glu	Gly	Ser	Ile	Glu	Glu	Asn	Phe	Leu	Gln	Phe	
124		370				375				380							
126	ctt	cag	ggg	act	ggc	tgt	cct	tct	gag	tcc	tgg	gtt	tcc	cga	ccc	cta	1200
127	Leu	Gln	Gly	Thr	Gly	Cys	Pro	Ser	Glu	Ser	Trp	Val	Ser	Arg	Pro	Leu	

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128 385          390          395          400
130 ccc agc ccc aag cag gag cca cct gct gtt gac ttt cga atc cca ggc      1248
131 Pro Ser Pro Lys Gln Glu Pro Pro Ala Val Asp Phe Arg Ile Pro Gly
132          405          410          415
134 cag ata gct gag gag acc tct gag ttc ctg gag cag caa ctc acc agc      1296
135 Gln Ile Ala Glu Glu Thr Ser Glu Phe Leu Glu Gln Gln Leu Thr Ser
136          420          425          430
138 gac atc atc atg tca gac agc tac ctc cgt cct gcc gcc tca ccc cgg      1344
139 Asp Ile Ile Met Ser Asp Ser Tyr Leu Arg Pro Ala Ala Ser Pro Arg
140          435          440          445
142 ctg gag tca tga      1356
143 Leu Glu Ser
144          450
147 <210> SEQ ID NO: 2
148 <211> LENGTH: 451
149 <212> TYPE: PRT
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158 Gly Arg Val Pro Gln Thr Pro Gly Pro Ser Thr Ala Ser Gly Val Pro
159          20          25          30
162 Glu Val Gly Leu Arg Asp Val Ala Ser Glu Ser Val Ala Leu Phe Phe
163          35          40          45
166 Met Leu Leu Leu Asp Leu Thr Ala Val Ala Gly Asn Ala Ala Val Met
167          50          55          60
170 Ala Val Ile Ala Lys Thr Pro Ala Leu Arg Lys Phe Val Phe Val Phe
171 65          70          75          80
174 His Leu Cys Leu Val Asp Leu Leu Ala Ala Leu Thr Leu Met Pro Leu
175          85          90          95
178 Ala Met Leu Ser Ser Ser Ala Leu Phe Asp His Ala Leu Phe Gly Glu
179          100          105          110
182 Val Ala Cys Arg Leu Tyr Leu Phe Leu Ser Val Cys Phe Val Ser Leu
183          115          120          125
186 Ala Ile Leu Ser Val Ser Ala Ile Asn Val Glu Arg Tyr Tyr Tyr Val
187          130          135          140
190 Val His Pro Met Arg Tyr Glu Val Arg Met Thr Leu Gly Leu Val Ala
191 145          150          155          160
194 Ser Val Leu Val Gly Val Trp Val Lys Ala Leu Ala Met Ala Ser Val
195          165          170          175
198 Pro Val Leu Gly Arg Val Ser Trp Glu Gly Ala Pro Ser Val Pro
199          180          185          190
202 Pro Gly Cys Ser Leu Gln Trp Ser His Ser Ala Tyr Cys Gln Leu Phe
203          195          200          205
206 Val Val Val Phe Ala Val Leu Tyr Phe Leu Leu Pro Leu Leu Leu Ile
207          210          215          220
210 Leu Val Val Tyr Cys Ser Met Phe Arg Val Ala Arg Val Ala Ala Met
211 225          230          235          240
214 Gln His Gly Pro Leu Pro Thr Trp Met Glu Thr Pro Arg Gln Arg Ser

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PATENT APPLICATION: US/10/079,384

TIME: 13:32:11

Input Set : A:\Seq listing 9409-2135.txt

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218	Glu Ser Leu Ser Ser Arg Ser Thr Met Val Thr Ser Ser Gly Ala Pro						
219		260		265		270	
222	Gln Thr Thr Pro His Arg Thr Phe Gly Gly Gly Lys Ala Ala Val Val						
223		275		280		285	
226	Leu Leu Ala Val Gly Gly Gln Phe Leu Leu Cys Trp Leu Pro Tyr Phe						
227		290		295		300	
230	Ser Phe His Leu Tyr Val Ala Leu Ser Ala Gln Pro Ile Ser Thr Gly						
231	305		310		315		320
234	Gln Val Glu Ser Val Val Thr Trp Ile Gly Tyr Phe Cys Phe Thr Ser						
235		325		330		335	
238	Asn Pro Phe Phe Tyr Gly Cys Leu Asn Arg Gln Ile Arg Gly Glu Leu						
239		340		345		350	
242	Ser Lys Gln Phe Val Cys Phe Phe Lys Pro Ala Pro Glu Glu Leu						
243		355		360		365	
246	Arg Leu Pro Ser Arg Glu Gly Ser Ile Glu Glu Asn Phe Leu Gln Phe						
247		370		375		380	
250	Leu Gln Gly Thr Gly Cys Pro Ser Glu Ser Trp Val Ser Arg Pro Leu						
251	385		390		395		400
254	Pro Ser Pro Lys Gln Glu Pro Pro Ala Val Asp Phe Arg Ile Pro Gly						
255		405		410		415	
258	Gln Ile Ala Glu Glu Thr Ser Glu Phe Leu Glu Gln Gln Leu Thr Ser						
259		420		425		430	
262	Asp Ile Ile Met Ser Asp Ser Tyr Leu Arg Pro Ala Ala Ser Pro Arg						
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266	Leu Glu Ser						
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271	<211> LENGTH 969						
272	<212> TYPE: DNA						
273	<213> ORGANISM: Homo sapiens						
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276	<221> NAME/KEY: CDS						
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278	<223> OTHER INFORMATION:						
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283	1	5		10		15	
285	gga act gag gag act ctt tgc tac aag cag acc ttg agc ctc acg gtg					96	
286	Gly Thr Glu Glu Thr Leu Cys Tyr Lys Gln Thr Leu Ser Leu Thr Val						
287		20		25		30	
289	ctg acg tgc atc gtt tcc ctt gtc ggg ctg aca gga aac gca gtt gtg					144	
290	Leu Thr Cys Ile Val Ser Leu Val Gly Leu Thr Gly Asn Ala Val Val						
291		35		40		45	
293	ctc tgg ctc ctg ggc tgc cgc atg cgc agg aac gcc ttc tcc atc tac					192	
294	Leu Trp Leu Leu Gly Cys Arg Met Arg Arg Asn Ala Phe Ser Ile Tyr						
295		50		55		60	
297	atc ctc aac ttg gcc gca gca gac ttc ctc ttc ctc agc ggc cgc ctt					240	

RAW SEQUENCE LISTING

DATE 07/29/2002

PATENT APPLICATION: US/10/079,384

TIME: 13 32:11

Input Set : A:\Seq listing 9409-2135.txt

Output Set: N:\CRF3\07292002\J079384.raw

298	Ile	Leu	Asn	Leu	Ala	Ala	Ala	Asp	Phe	Leu	Phe	Leu	Ser	Gly	Arg	Leu	
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302	Ile	Tyr	Ser	Leu	Leu	Ser	Phe	Ile	Ser	Ile	Pro	His	Thr	Ile	Ser	Lys	
303				85					90					95			
305	atc	ctc	tat	cct	gtg	atg	atg	ttt	tcc	tac	ttt	gca	ggc	ctg	agc	ttt	336
306	Ile	Leu	Tyr	Pro	Val	Met	Met	Phe	Ser	Tyr	Phe	Ala	Gly	Leu	Ser	Phe	
307				100					105					110			
309	ctg	agt	gcc	gtg	agc	acc	gag	cgc	tgc	ctg	tcc	gtc	ctg	tgg	ccc	atc	384
310	Leu	Ser	Ala	Val	Ser	Thr	Glu	Arg	Cys	Leu	Ser	Val	Leu	Trp	Pro	Ile	
311			115					120					125				
313	tgg	tac	cgc	tgc	cac	cgc	ccc	aca	cac	ctg	tca	gcg	gtg	gtg	tgt	gtc	432
314	Trp	Tyr	Arg	Cys	His	Arg	Pro	Thr	His	Leu	Ser	Ala	Val	Val	Cys	Val	
315		130				135					140						
317	ctg	ctc	tgg	gcc	ctg	tcc	ctg	ctg	cgg	agc	atc	ctg	gag	tgg	atg	tta	480
318	Leu	Leu	Trp	Ala	Leu	Ser	Leu	Leu	Arg	Ser	Ile	Leu	Glu	Trp	Met	Leu	
319	145				150				155					160			
321	tgt	ggc	ttc	ctg	ttc	agt	ggt	gct	gat	tct	gct	tgg	tgt	caa	aca	tca	528
322	Cys	Gly	Phe	Leu	Phe	Ser	Gly	Ala	Asp	Ser	Ala	Trp	Cys	Gln	Thr	Ser	
323			165					170					175				
325	gat	ttc	atc	aca	gtc	gcg	tgg	ctg	att	ttt	tta	tgt	gtg	gtt	ctc	tgt	576
326	Asp	Phe	Ile	Thr	Val	Ala	Trp	Leu	Ile	Phe	Leu	Cys	Val	Val	Leu	Cys	
327			180					185					190				
329	ggg	tcc	agc	ctg	gtc	ctg	ctg	atc	agg	att	ctc	tgt	gga	tcc	cgg	aag	624
330	Gly	Ser	Ser	Leu	Val	Leu	Leu	Ile	Arg	Ile	Leu	Cys	Gly	Ser	Arg	Lys	
331		195				200					205						
333	ata	ccg	ctg	acc	agg	ctg	tac	gtg	acc	atc	ctg	ctc	aca	gta	ctg	gtc	672
334	Ile	Pro	Leu	Thr	Arg	Leu	Tyr	Val	Thr	Ile	Leu	Leu	Thr	Val	Leu	Val	
335		210				215					220						
337	ttc	ctc	ctc	tgt	ggc	ctg	ccc	ttt	ggc	att	cag	ttt	ttc	cta	ttt	tta	720
338	Phe	Leu	Leu	Cys	Gly	Leu	Pro	Phe	Gly	Ile	Gln	Phe	Phe	Leu	Phe	Leu	
339	225				230				235					240			
341	tgg	atc	cac	gtg	gac	agg	gaa	gtc	tta	ttt	tgt	cat	gtt	cat	cta	gtt	768
342	Trp	Ile	His	Val	Asp	Arg	Glu	Val	Leu	Phe	Cys	His	Val	His	Leu	Val	
343			245					250					255				
345	tct	att	ttc	ctg	tcc	gct	ctt	aac	agc	agt	gcc	aac	ccc	atc	att	tac	816
346	Ser	Ile	Phe	Leu	Ser	Ala	Leu	Asn	Ser	Ser	Ala	Asn	Pro	Ile	Ile	Tyr	
347			260					265					270				
349	ttc	ttc	gtg	ggc	tcc	ttt	agg	cag	cgt	caa	aat	agg	cag	aac	ctg	aag	864
350	Phe	Phe	Val	Gly	Ser	Phe	Arg	Gln	Arg	Gln	Asn	Arg	Gln	Asn	Leu	Lys	
351		275				280					285						
353	ctg	gtt	ctc	cag	agg	gct	ctg	cag	gac	gcg	tct	gag	gtg	gat	gaa	ggt	912
354	Leu	Val	Leu	Gln	Arg	Ala	Leu	Gln	Asp	Ala	Ser	Glu	Val	Asp	Glu	Gly	
355		290				295					300						
357	gga	ggg	cag	ctt	cct	gag	gaa	atc	ctg	gag	ctg	tcg	gga	agc	aga	ttg	960
358	Gly	Gly	Gln	Leu	Pro	Glu	Glu	Ile	Leu	Glu	Leu	Ser	Gly	Ser	Arg	Leu	
359	305				310				315					320			
361	gag	cag	tga														964
362	Glu	Gln															

RAW SEQUENCE LISTING ERROR SUMMARY DATE 07/29/2002
PATENT APPLICATION: US/10/079,384 TIME 13:32:12

Input Set : A:\Seq listing 9409-2135.txt
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:35; Xaa Pos. 1,4

Seq#:36; Xaa Pos. 1,4,8

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/079,384

DATE: 07/29/2002

TIME: 13:32:12

Input Set : A:\Seq listing 9409-2135.txt

Output Set: N:\CRF3\07292002\J079384.raw

L:2968 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35 after pos.:0
L:3008 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:36 after pos.:0